



ATTACHMENTS:

1) Corrected Sequence Listing



1

SEQUENCE LISTING

<110> ASAKO, HIROYUKI
MATSUMURA, KENJI
SHIMIZU, MASATOSHI
ITO, NOBUYA
WAKITA, RYUHEI

<120> PROCESS FOR PRODUCING OPTICALLY ACTIVE
4-HALO-3-HYDROXYBUTANOATE

<130> 7372-72249

<140> 10/004,115
<141> 2001-12-06

<150> JP 2000-372704
<151> 2000-12-07

<150> JP 2001-006144
<151> 2001-01-15

<150> JP 2001-026594
<151> 2001-02-02

<150> JP 2001-175175
<151> 2001-06-11

<160> 37

<170> PatentIn Ver. 3.2

<210> 1
<211> 325
<212> PRT
<213> Penicillium citrinum

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Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro
1 5 10 15

Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
20 25 30

Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
35 40 45

Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
50 55 60

Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
65 70 75 80

Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
85 90 95

Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
100 105 110

Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
 115 120 125
 Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
 130 135 140
 Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
 145 150 155 160
 Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
 165 170 175
 Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
 180 185 190
 Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
 195 200 205
 Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
 210 215 220
 Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
 225 230 235 240
 Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
 245 250 255
 Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
 260 265 270
 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
 275 280 285
 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
 290 295 300
 Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala
 305 310 315 320
 Lys Asn Leu Ser Ala
 325

<210> 2
 <211> 978
 <212> DNA
 <213> Penicillium citrinum

<220>
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 1 5 10 15

ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc		96	
Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr			
20	25	30	
tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac		144	
Tyr Thr Ala Val Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp			
35	40	45	
tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt		192	
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg			
50	55	60	
gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc		240	
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val			
65	70	75	80
tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg		288	
Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp			
85	90	95	
tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg		336	
Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met			
100	105	110	
ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag		384	
Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu			
115	120	125	
ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc		432	
Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr			
130	135	140	
gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat		480	
Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp			
145	150	155	160
cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt		528	
Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu			
165	170	175	
gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc		576	
Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile			
180	185	190	
gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc		624	
Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe			
195	200	205	
tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac		672	
Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn			
210	215	220	
cag gtt ccc acc acc ggt gag cggt gtc agc gag aac aag act ctg aac		720	
Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn			
225	230	235	240

gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc		768	
Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala			
245	250	255	
tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc		816	
Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro			
260	265	270	
aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac		864	
Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp			
275	280	285	
ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc		912	
Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val			
290	295	300	
aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc		960	
Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala			
305	310	315	320
aag aac ctg tct gcg tga		978	
Lys Asn Leu Ser Ala			
325			

<210> 3

<211> 17

<212> PRT

<213> Penicillium citrinum

<400> 3

Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn Gln Val			
1	5	10	15

Pro

<210> 4

<211> 10

<212> PRT

<213> Penicillium citrinum

<400> 4

Ile Pro Gly Val Phe Gly Thr Phe Ala Ser		
1	5	10

<210> 5

<400> 5

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<210> 6

<211> 14

<212> PRT

<213> Penicillium citrinum

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<221> MOD_RES
<222> (6)..(7)
<223> Variable amino acid

<400> 6
Tyr Glu Asp Val Leu Xaa Xaa Ile Asp Asp Ser Leu Lys Arg
1           5           10

<210> 7

<400> 7
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<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
ggaacytgrt tytggsacc                                         20

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
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<222> (3)
<223> a, c, t, g, other or unknown

<220>
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<222> (6)
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<220>
<221> modified_base
<222> (9)
<223> a, c, t, g, other or unknown

<400> 9
tangcnacng gcataatatt                                         20

<210> 10
<211> 20
<212> DNA
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<213> Artificial Sequence  
  
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<223> a, c, t, g, other or unknown  
  
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<223> a, c, t, g, other or unknown  
  
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<400> 10  
tangcnacng gcataatgtt
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<210> 11  
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<210> 12  
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<400> 12
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20

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<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
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<220>
<221> modified_base
<222> (9)
<223> a, c, t, g, other or unknown

<400> 13
tangcnacng gcattatat
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<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer
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<400> 14
tangcnacng gcattatgtt
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<210> 15
<211> 697
<212> DNA
<213> Escherichia coli

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aanactttca cactgagcaa cggcgtcaaa attccctggcg tcggcttgg tacctncgct 120
agtgaagggtt ccaagggcga aacctatnct gctgtcacca ctgccctgaa aaccgggtac 180
cgtncttgg actgtgcctg gtactacctg aacaagggtg aggttggtga gggtntccgt 240
gacttcctga aggaaaaccc ctcgggtgaag cgtgaggaca tcttcgtctg caccagggtg 300
tggaaccacc tccaccgtta tgaggacgtc ctctggtcca ttgacnactc cctgaagegt 360
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cttggacttg actacgttga tatgttcctc gttcaactggc ccattgctgc cgaaaaaaaaat 420
ggccagggtg agccccaaaat tggccctgac ggcaaatacn tcnttctcaa ggacctgacc 480
gaaancccna ncccacctgg cgcgctatgg aaaaaatttn tgangatccc aaggccaggt 540
ccattggtgt ttccaatttg accatgccc accttgagaa gatgtccaag ttngccaagg 600
tnatgcctca cgccaaccag atcgagattc acccccttct gcccaacgag gagctggtgc 660
agtactgctt ttccaagaac antatgccc tagcgta 697

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<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
ggaggtggtt ccacacacctt g

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21

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<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
caaccagatc gagattcacc

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20

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<210> 18
<211> 331
<212> DNA
<213> Escherichia coli

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<222> (14)
<223> a, c, t, g, other or unknown

<400> 18
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cccatcatgt ctaacggaaa gactttcaca ttgagcaacg gcgtaagat tcctggcgtc 120
ggctttggta cttcgctag tgaaggttcc aaggggcgaga cctataactgc tgtcaccact 180
gccctgaaga ccggttaccg tcacttggac tttgcctgggt actacctgaa cgagggtgag 240
gttggtgagg gtatccgtga cttcctgaag gagaacccct cggtaagcg tgaggacatc 300
ttcgtctgca ccaagggtgtg gaaccacctc c

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331

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<210> 19
<211> 743
<212> DNA
<213> Escherichia coli

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<222> (639)
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<222> (648)
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<220>
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<222> (651)..(652_
<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (659)
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<220>
<221> modified_base
<222> (662)
<223> a, c, t, g, other or unknown
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<221> modified_base
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<222> (690)
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<222> (702)
<223> a, c, t, g, other or unknown

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<221> modified_base
<222> (717)
<223> a, c, t, g, other or unknown

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<221> modified_base
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<223> a, c, t, g, other or unknown

<220>
<221> modified_base
<222> (734)
<223> a, c, t, g, other or unknown

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caagaacatt atgcccgtgg cctactctcc tctgggctcg cagaaccagg ttccccaccac 120
cggtgagcgg gtcagcgaga acaagactct gaacgagatc gccgagaagg gccggcaacac 180
ccttgctcag gtttttattt cctgggtct ggcggcgtgg tacgtcggtt tcggcaagag 240
ctccaacccc aagcgcatgt agtccaactt caagagcatt gagctctccg atgcccactt 300
tgaaggccatc aatggccgttg ccaagggtcg tcacttccgt ttctgtcaaca tgaaggatac 360
tttcggatat gatgtctggc ccgaggagac cgccaaagaac ctgtctcggt gaatctctac 420

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gaaattataa aatnacaccn acnaaaaancc aaagcgaaag gatgatnccc aaaantttt 480
 agggttctt gtttgcggaaac gtttgcggaaac gtttgcggaaac gtttgcggaaac gtttgcggaaac 540
 tctccaaaaaa aaaaaaaaaaa aaaaacggtc cgcggccgct ccnnnggggg gccccgttcc 600
 caattcnccc cttatnattt aattttttt taanggggncc aaattccncc nnatttccnt 660
 cnanattgggn nggccgcctc caaacttccn tcntnaaagg gncccaattc ccccccattt 720
 aantggattt cctntttacc ttt 743

<210> 20
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 20
 ccaagggttg gaaccacccctc c

21

<210> 21
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 21
 ccagaggaga gtaggccacg g

21

<210> 22
 <211> 417
 <212> DNA
 <213> Escherichia coli

 <400> 22
 ccaagggttg gaaccacccctc caccgttatg aggacgtcct ctggccatt gacgactccc 60
 tgaaggcgtct tggacttgc tacgttgcata tggccatcgat tcactggccc attgctgccc 120
 agaagaatgg ccagggttag cccaaatgg gcctgacgg caaatacgtc attctcaagg 180
 acctgaccga gaaccccgag cccacatggc gcgctatgg aagattt gaggatcgca 240
 agggccaggta cattgggtgc tccaactggc ccattggccga cttggaaatg atgtccaagt 300
 tcggccaaaggta catgcctcac gccaaccaga tcgagattca ccccttcctg cccaaacgagg 360
 agctggtgca gtactgcttc tccaagaaca ttatggccgt ggcctactct cctctgg 417

<210> 23
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 23
 gccatggcta tgtctaacgg aaagact

27

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<210> 24
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
cgatccgtt ataatttcgt agagattca

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29

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<210> 25
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
gatcatcata gcaggagtca t

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21

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<210> 26
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
gaattcaaca ccagtcagct c

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21

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<210> 27
<211> 786
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(783)

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<400> 27
atg tat aaa gat tta gaa gga aaa gta gtt gtc ata aca ggt tca tct 48
Met Tyr Lys Asp Leu Glu Gly Lys Val Val Val Ile Thr Gly Ser Ser
   1      5          10           15

```

```

acc ggt tta gga aaa gca atg gcg att cgt ttt gcg aca gaa aaa gct 96
Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala
   20      25          30

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```

aaa gta gtt gtg aac tat cgt tcg aaa gaa gaa gct aac agc gtt 144
Lys Val Val Asn Tyr Arg Ser Lys Glu Glu Ala Asn Ser Val
   35      40           45

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tta gaa gaa att aaa aaa gtg ggc gga gag gct att gcc gtc aaa ggt Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly	192
50 55 60	
gat gta aca gtt gag tct gat gtg atc aat tta gtt caa tct gct att Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile	240
65 70 75 80	
aaa gaa ttt gga aag cta gac gtt atg att aat aac gca gga atg gaa Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu	288
85 90 95	
aat ccg gtt tcg tct cat gaa atg tct tta agt gat tgg aat aaa gtc Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val	336
100 105 110	
att gat acg aac tta acg gga gca ttt tta ggc agc cgt gaa gcg att Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile	384
115 120 125	
aaa tat ttt gtg gaa aat gat att aag gga aca gtt att aac atg tcg Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser	432
130 135 140	
agt gtt cac gag aaa att cct tgg cca tta ttt gtt cat tac gca gca Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala	480
145 150 155 160	
agt aaa ggc gga atg aag ctc atg acc gaa aca ctt gca tta gaa tac Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr	528
165 170 175	
gct cca aaa ggt att cgt gta aat aac att gga ccg gga gcg att aat Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn	576
180 185 190	
aca ccg att aac gct gag aaa ttt gct gat cct gag cag cgt gca gat Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp	624
195 200 205	
gta gaa agc atg att cca atg gga tac att gga gag ccg gaa gaa att Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile	672
210 215 220	
gca gcg gtt gct gca tgg cta gct tct tca gag gca agt tat gta aca Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr	720
225 230 235 240	
ggg att aca ctc ttt gct gac ggc ggt atg aca cag tac cca tca ttc Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe	768
245 250 255	
caa gca gga cgc gga taa Gln Ala Gly Arg Gly	786
260	

<210> 28
 <211> 996
 <212> DNA
 <213> Penicillium citrinum

 <220>
 <221> CDS
 <222> (1)...(975)

 <400> 28
 atg tct aac gga aag act ttc aca ttg agc aac ggc gtc aag att cct 48
 Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro
 1 5 10 15

 ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc 96
 Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
 20 25 30

 tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac 144
 Tyr Thr Ala Val Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
 35 40 45

 tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt 192
 Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
 50 55 60

 gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc 240
 Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
 65 70 75 80

 tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg 288
 Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
 85 90 95

 tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg 336
 Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
 100 105 110

 ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag 384
 Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
 115 120 125

 ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc 432
 Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
 130 135 140

 gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat 480
 Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
 145 150 155 160

 cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt 528
 Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
 165 170 175

 gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc 576
 Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
 180 185 190

gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe 195 200 205	624
tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn 210 215 220	672
cag gtt ccc acc acc ggt gag cggt gtc agc gag aac aag act ctg aac Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn 225 230 235 240	720
gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala 245 250 255	768
tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro 260 265 270	816
aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp 275 280 285	864
ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val 290 295 300	912
aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala 305 310 315 320	960
aag aac ctg tct gcg tgaatctcta cgaaattata a Lys Asn Leu Ser Ala 325	996

<210> 29
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer
<400> 29
cggatccgtt cacgcagaca ggttcttgg

29

<210> 30
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 30
gccatggcta tgtataaaga tttagaa

27

<210> 31

<400> 31
000

<210> 32
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 32
cggatccgtt atccgcgtcc tgc

23

<210> 33
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 33
cggatccgag cgcccaatac gcaaaccg

28

<210> 34
<211> 348
<212> PRT
<213> Corynebacterium sp.

<400> 34
Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr
1 5 10 15

Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
20 25 30

Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro
35 40 45

Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly
50 55 60

Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile
65 70 75 80

Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp
85 90 95

His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu
 100 105 110

Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
 115 120 125

Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
 130 135 140

Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
 145 150 155 160

Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val
 165 170 175

Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
 180 185 190

His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
 195 200 205

Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
 210 215 220

Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala
 225 230 235 240

Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala
 245 250 255

Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
 260 265 270

Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
 275 280 285

Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu
 290 295 300

Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Ser Val Glu Thr
 305 310 315 320

Phe Ser Leu Asp Asn Gly Ala Glu Ala Tyr Arg Arg Leu Ala Ala Gly
 325 330 335

Thr Leu Ser Gly Arg Ala Val Val Pro Gly Leu
 340 345

<210> 35
 <211> 1047
 <212> DNA
 <213> Corynebacterium sp.

<220>
 <221> CDS
 <222> (1)...(1044)

<400> 35
atg aag gcg atc cag tac acg aga atc ggc gcg gaa ccc gaa ctc acg 48
Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr
1 5 10 15

gag att ccc aaa ccc gag ccc ggt cca ggt gaa gtg ctc ctg gaa gtc 96
Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
20 25 30

acc gct gct ggc gtc tgc cac tcg gac gac ttc atc atg agc ctg ccc 144
Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro
35 40 45

gaa gag cag tac acc tac ggc ctt ccg ctc acg ctc ggc cac gaa ggc 192
Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly
50 55 60

gca ggc aag gtc gcc gtc ggc gag ggt gtc gaa ggt ctc gac atc 240
Ala Gly Lys Val Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile
65 70 75 80

gga acc aat gtc gtc gtc tac ggg cct tgg ggt tgc ggc aac tgt tgg 288
Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp
85 90 95

cac tgc tca caa gga ctc gag aac tat tgc tct cgc gcc caa gaa ctc 336
His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu
100 105 110

gga atc aat cct ccc ggt ctc ggt gca ccc ggc gcg ttg gcc gag ttc 384
Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
115 120 125

atg atc gtc gat tct cct cgc cac ctt gtc ccg atc ggt gac ctc gac 432
Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
130 135 140

ccg gtc aag acg gtg ccg ctg acc gac gcc ggt ctg acg ccg tat cac 480
Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
145 150 155 160

gcg atc aag cgt tct ctg ccg aaa ctt cgc gga ggc tcg tac gcg gtt 528
Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val
165 170 175

gtc att ggt acc ggc ggt ctc ggc cac gtc gct att cag ctc ctc cgc 576
Val Ile Gly Thr Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
180 185 190

cac ctc tcg gcg gca acg gtc atc gct ttg gac gtg agc gcg gac aag 624
His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
195 200 205

ctc gaa ctg gca acc aag gta ggc gct cac gaa gtg gtt ctg tcc gac 672
Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
210 215 220

aag gac gcg gcc gag aac gtc cgc aag atc act gga agt caa ggc gcc	720
Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala	
225 230 235 240	240
gca ttg gtt ctc gac ttc gtc ggc tac cag ccc acc atc gac acc gcg	768
Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala	
245 250 255	255
atg gct gtc gcc ggc gtc gga tca gac gtc acg atc gtc ggg atc ggg	816
Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly	
260 265 270	270
gac ggc cag gcc cac gcc aaa gtc ggg ttc ttc caa agt cct tac gag	864
Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu	
275 280 285	285
gct tcg gtg aca gtc ccg tat tgg ggt gcc cgc aac gag ttg atc gaa	912
Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu	
290 295 300	300
ttg atc gac ctc gcc cac gcc ggc atc ttc gac atc tcg gtg gag acc	960
Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Ser Val Glu Thr	
305 310 315 320	320
ttc agt ctc gac aac ggt gcc gaa gcg tat cga cga ctg gct gcc gga	1008
Phe Ser Leu Asp Asn Gly Ala Glu Ala Tyr Arg Arg Leu Ala Ala Gly	
325 330 335	335
acg ctc agc ggc cgt gcg gtt gtg gtc cct ggt ctg tag	1047
Thr Leu Ser Gly Arg Ala Val Val Val Pro Gly Leu	
340 345	345

<210> 36
<211> 261
<212> PRT
<213> Escherichia coli

<400> 36	
Met Tyr Lys Asp Leu Glu Gly Lys Val Val Val Ile Thr Gly Ser Ser	
1 5 10 15	15
Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala	
20 25 30	30
Lys Val Val Val Asn Tyr Arg Ser Lys Glu Glu Glu Ala Asn Ser Val	
35 40 45	45
Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly	
50 55 60	60
Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile	
65 70 75 80	80
Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu	
85 90 95	95

Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val
100 105 110

Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
115 120 125

Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser
130 135 140

Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145 150 155 160

Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
165 170 175

Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
180 185 190

Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp
195 200 205

Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
210 215 220

Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr
225 230 235 240

Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
245 250 255

Gln Ala Gly Arg Gly
260

<210> 37

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 37

Trp Ile Ser Thr Lys Leu

1 5